

SEQUENCE LISTING

(1) GENERAL INFORMATION:

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(i) APPLICANT: Tryggvason, Karl
Kestila, Marjo
Lenkkeri, Ulla
Mannikko, Minna

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(ii) TITLE OF INVENTION: Neph rin Gene and Protein

(iii) NUMBER OF SEQUENCES: 6

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(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
(B) STREET: 300 S. Wacker Drive, Suite 3200
(C) CITY: Chicago
(D) STATE: IL
(E) COUNTRY: USA
(F) ZIP: 60606

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

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(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

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(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Chao, Mark
(B) REGISTRATION NUMBER: 37,293
(C) REFERENCE/DOCKET NUMBER: 97,842

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(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (312)913-0001
(B) TELEFAX: (312)913-0002

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(2) INFORMATION FOR SEQ ID NO:1:

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(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 4285 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: not relevant

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(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 1..66
 (D) OTHER INFORMATION: /note= "putative signal peptide"

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..3723

(ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 67..3723

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 121..122
 (D) OTHER INFORMATION: /note= "deletion mutation
 FIN-Major"

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 3800..3804
 (D) OTHER INFORMATION: /note= "nonsense mutation in exon
 26 FIN-Minor"

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 3178..3258
 (D) OTHER INFORMATION: /note= "putative transmembrane
 domain"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

35	ATG GCC CTG GGG ACG ACG CTC AGG GCT TCT CTC CTG CTC CTG GGG CTG	48
	Met Ala Leu Gly Thr Thr Leu Arg Ala Ser Leu Leu Leu Leu Gly Leu	
	-22 -20 -15 -10	
40	CTG ACT GAA GGC CTG GCG CAG TTG GCG ATT CCT GCC TCC GTT CCC CGG	96
	Leu Thr Glu Gly Leu Ala Gln Leu Ala Ile Pro Ala Ser Val Pro Arg	
	-5 1 5 10	
45	GGC TTC TGG GCC CTG CCT GAA AAC CTG ACG GTG GTG GAG GGG GCC TCA	144
	Gly Phe Trp Ala Leu Pro Glu Asn Leu Thr Val Val Glu Gly Ala Ser	
	15 20 25	
50	GTG GAG CTG CGT TGT GGG GTC AGC ACC CCT GGC AGT GCG GTG CAA TGG	192
	Val Glu Leu Arg Cys Gly Val Ser Thr Pro Gly Ser Ala Val Gln Trp	
	30 35 40	
55	GCC AAA GAT GGG CTG CTC CTG GGC CCC GAC CCC AGG ATC CCA GGC TTC	240
	Ala Lys Asp Gly Leu Leu Leu Gly Pro Asp Pro Arg Ile Pro Gly Phe	
	45 50 55	
	CCG AGG TAC CGC CTG GAA GGG GAC CCT GCT AGA GGT GAA TTC CAC CTG	288
	Pro Arg Tyr Arg Leu Glu Gly Asp Pro Ala Arg Gly Glu Phe His Leu	

	60	65	70	
5	CAC ATC GAG GCC TGT GAC His Ile Glu Ala Cys Asp 75 80	CTC AGC GAT GAC GCG Leu Ser Asp Asp Ala Glu 85	GAG TAT GAG TGC CAG Tyr Glu Cys Gln 90	336
10	GTC GGC CGC TCT GAG ATG GGG CCC Val Gly Arg Ser Glu Met Gly Pro 95 100	GAG CTC GTG TCT CCC AGA GTG ATC Glu Leu Val Ser Pro Arg Val Ile 105		384
15	CTC TCC ATC CTG GTT CCT CCC AAG CTG CTC CTG CTG ACC CCA GAG GCA Leu Ser Ile Leu Val Pro Pro Lys Leu Leu Leu Leu Thr Pro Glu Ala 110 115 120			432
20	GGC ACC ATG GTC ACC TGG GTA GCT GGG CAG GAG TAC GTG GTC AAC TGT Gly Thr Met Val Thr Trp Val Ala Gly Gln Glu Tyr Val Val Asn Cys 125 130 135			480
25	GTG TCT GGG GAC GCG AAG CCA GCA CCT GAC ATC ACC ATT CTC CTG AGT Val Ser Gly Asp Ala Lys Pro Ala Pro Asp Ile Thr Ile Leu Leu Ser 140 145 150			528
30	GGA CAG ACA ATA TCT GAC ATC TCT GCA AAC GTG AAC GAG GGC TCC CAG Gly Gln Thr Ile Ser Asp Ile Ser Ala Asn Val Asn Glu Gly Ser Gln 155 160 165 170			576
35	CAG AAA CTC TTC ACT GTG GAG GCC ACA GCC AGG GTG ACA CCC CGG AGC Gln Lys Leu Phe Thr Val Glu Ala Thr Ala Arg Val Thr Pro Arg Ser 175 180 185			624
40	TCA GAT AAT AGG CAG TTG CTG GTC TGT GAG GCG TCT AGC CCA GCA CTG Ser Asp Asn Arg Gln Leu Leu Val Cys Glu Ala Ser Ser Pro Ala Leu 190 195 200			672
45	GAG GCC CCC ATC AAG GCC TCA TTC ACC GTG AAT GTT CTG TTC CCT CCA Glu Ala Pro Ile Lys Ala Ser Phe Thr Val Asn Val Leu Phe Pro Pro 205 210 215			720
50	GGA CCC CCT GTC ATC GAG TGG CCA GGC CTG GAT GAG GGG CAC GTG CGG Gly Pro Pro Val Ile Glu Trp Pro Gly Leu Asp Glu Gly His Val Arg 220 225 230			768
55	GCA GGA CAG AGC TTG GAG CTG CCG TGC GTG GCC CGA GGG GGT AAT CCC Ala Gly Gln Ser Leu Glu Leu Pro Cys Val Ala Arg Gly Gly Asn Pro 235 240 245 250			816
60	TTA GCC ACA CTG CAG TGG CTG AAG AAT GGC CAG CCG GTG TCC ACA GCG Leu Ala Thr Leu Gln Trp Leu Lys Asn Gly Gln Pro Val Ser Thr Ala 255 260 265			864
65	TGG GGC ACA GAG CAC ACC CAG GCG GTG GCC CGC AGT GTG CTG GTG ATG Trp Gly Thr Glu His Thr Gln Ala Val Ala Arg Ser Val Leu Val Met 270 275 280			912
70	ACC GTG AGG CCA GAA GAC CAT GGA GCG CAG CTC AGC TGC GAG GCC CAC Thr Val Arg Pro Glu Asp His Gly Ala Gln Leu Ser Cys Glu Ala His 285 290 295			960

	AAC AGC GTG TCT GCA GGG ACC CAG GAG CAC GGC ATC ACA CTG CAG GTC	1008
	Asn Ser Val Ser Ala Gly Thr Gln Glu His Gly Ile Thr Leu Gln Val	
	300 305 310	
5	ACC TTT CCC CCT AGT GCC ATT ATT ATC TTG GGA TCT GCA TCC CAG ACT	1056
	Thr Phe Pro Pro Ser Ala Ile Ile Ile Leu Gly Ser Ala Ser Gln Thr	
	315 320 325 330	
10	GAG AAC AAG AAC GTG ACA CTC TCC TGT GTC AGC AAG TCC AGT CGC CCG	1104
	Glu Asn Lys Asn Val Thr Leu Ser Cys Val Ser Lys Ser Ser Arg Pro	
	335 340 345	
15	CGG GTT CTG CTA CGA TGG TGG CTG GGC TGG CGG CAG CTG CTG CCC ATG	1152
	Arg Val Leu Leu Arg Trp Trp Leu Gly Trp Arg Gln Leu Leu Pro Met	
	350 355 360	
20	GAG GAG ACA GTC ATG GAT GGA CTG CAT GGC GGT CAC ATC TCC ATG TCC	1200
	Glu Glu Thr Val Met Asp Gly Leu His Gly Gly His Ile Ser Met Ser	
	365 370 375	
25	AAC CTG ACA TTC CTG GCG CGG CGG GAG GAC AAC GGT CTG ACC CTC ACA	1248
	Asn Leu Thr Phe Leu Ala Arg Arg Glu Asp Asn Gly Leu Thr Leu Thr	
	380 385 390	
30	TGT GAG GCC TTC AGT GAA GCC TTC ACC AAG GAG ACC TTC AAG AAG TCG	1296
	Cys Glu Ala Phe Ser Glu Ala Phe Thr Lys Glu Thr Phe Lys Lys Ser	
	395 400 405 410	
35	CTC ATC CTG AAC GTA AAA TAT CCC GCC CAG AAA CTG TGG ATT GAG GGT	1344
	Leu Ile Leu Asn Val Lys Tyr Pro Ala Gln Lys Leu Trp Ile Glu Gly	
	415 420 425	
40	CCC CCA GAG GGC CAG AAG CTC CGG GCT GGG ACC CGG GTG AGG CTG GTG	1392
	Pro Pro Glu Gly Gln Lys Leu Arg Ala Gly Thr Arg Val Arg Leu Val	
	430 435 440	
45	TGT TTG GCT ATC GGG GGC AAC CCA GAG CCC TCC CTC ATG TGG TAC AAG	1440
	Cys Leu Ala Ile Gly Gly Asn Pro Glu Pro Ser Leu Met Trp Tyr Lys	
	445 450 455	
50	GAC TCG CGC ACC GTG ACC GAG TCG CGG CTG CCG CAG GAG TCG CGG CGC	1488
	Asp Ser Arg Thr Val Thr Glu Ser Arg Leu Pro Gln Glu Ser Arg Arg	
	460 465 470	
55	GTG CAT CTC GGC AGC GTG GAG AAA TCT GGG AGC ACC TTC TCC CGA GAG	1536
	Val His Leu Gly Ser Val Glu Lys Ser Gly Ser Thr Phe Ser Arg Glu	
	475 480 485 490	
60	CTG GTG CTG GTC ACA GGG CCG TCG GAC AAC CAG GCC AAG TTC ACG TGC	1584
	Leu Val Leu Val Thr Gly Pro Ser Asp Asn Gln Ala Lys Phe Thr Cys	
	495 500 505	
65	AAG GCT GGA CAG CTC AGC GCG TCC ACG CAG CTG GCG GTG CAG TTT CCC	1632
	Lys Ala Gly Gln Leu Ser Ala Ser Thr Gln Leu Ala Val Gln Phe Pro	
	510 515 520	

	CCA	ACT	AAC	GTG	ACG	ATC	CTG	GCC	AAC	GCA	TCC	GCA	CTG	CGC	CCG	GGA	1680
	Pro	Thr	Asn	Val	Thr	Ile	Leu	Ala	Asn	Ala	Ser	Ala	Leu	Arg	Pro	Gly	
			525					530					535				
5	GAC	GCC	TTA	AAC	TTG	ACA	TGC	GTC	AGC	GTC	AGC	AGC	AAT	CCG	CCG	GTC	1728
	Asp	Ala	Leu	Asn	Leu	Thr	Cys	Val	Ser	Val	Ser	Ser	Asn	Pro	Pro	Val	
		540					545					550					
10	AAC	TTG	TCC	TGG	GAC	AAG	GAA	GGG	GAG	AGG	CTG	GAG	GGC	GTG	GCC	GCC	1776
	Asn	Leu	Ser	Trp	Asp	Lys	Glu	Gly	Glu	Arg	Leu	Glu	Gly	Val	Ala	Ala	
		555				560					565					570	
15	CCA	CCC	CGG	AGA	GCC	CCA	TTC	AAA	GGC	TCC	GCC	GCC	GCC	AGG	AGC	GTC	1824
	Pro	Pro	Arg	Arg	Ala	Pro	Phe	Lys	Gly	Ser	Ala	Ala	Ala	Arg	Ser	Val	
					575					580					585		
20	CTT	CTG	CAA	GTG	TCA	TCC	CGC	GAT	CAT	GGC	CAG	CGC	GTG	ACC	TGC	CGC	1872
	Leu	Leu	Gln	Val	Ser	Ser	Arg	Asp	His	Gly	Gln	Arg	Val	Thr	Cys	Arg	
				590					595					600			
25	GCC	CAC	AGC	GCC	GAG	CTC	CGC	GAA	ACC	GTG	AGC	TCC	TTC	TAT	CGC	CTC	1920
	Ala	His	Ser	Ala	Glu	Leu	Arg	Glu	Thr	Val	Ser	Ser		Phe	Tyr	Arg	
			605					610						615			
30	AAC	GTA	CTG	TAC	CGT	CCA	GAG	TTC	CTG	GGG	GAG	CAG	GTG	CTG	GTG	GTG	1968
	Asn	Val	Leu	Tyr	Arg	Pro	Glu	Phe	Leu	Gly	Glu	Gln	Val	Leu	Val	Val	
		620					625					630					
35	ACC	GCG	GTG	GAG	CAG	GGC	GAG	GCG	TTG	CTG	CCC	GTG	TCC	GTG	TCC	GCT	2016
	Thr	Ala	Val	Glu	Gln	Gly	Glu	Ala	Leu	Leu	Pro	Val	Ser	Val	Ser	Ala	
		635				640					645					650	
40	AAC	CCC	GCC	CCC	GAG	GCC	TTC	AAC	TGG	ACC	TTC	CGC	GGC	TAT	CGC	CTC	2064
	Asn	Pro	Ala	Pro	Glu	Ala	Phe	Asn	Trp	Thr	Phe	Arg	Gly	Tyr	Arg	Leu	
				655						660					665		
45	AGT	CCA	GCG	GGC	GGC	CCC	CGG	CAT	CGC	ATC	CTG	TCC	AGC	GGG	GCT	CTG	2112
	Ser	Pro	Ala	Gly	Gly	Pro	Arg	His	Arg	Ile	Leu	Ser	Ser	Gly	Ala	Leu	
				670					675					680			
50	CAT	CTG	TGG	AAT	GTG	ACC	CGC	GCG	GAC	GAC	GGC	CTC	TAT	CAG	CTG	CAC	2160
	His	Leu	Trp	Asn	Val	Thr	Arg	Ala	Asp	Asp	Gly	Leu	Tyr	Gln	Leu	His	
			685					690					695				
55	TGC	CAG	AAC	TCT	GAG	GGC	ACC	GCG	GAA	GCG	CGG	CTG	CGG	CTG	GAC	GTG	2208
	Cys	Gln	Asn	Ser	Glu	Gly	Thr	Ala	Glu	Ala	Arg	Leu	Arg	Leu	Asp	Val	
		700					705					710					
60	CAC	TAT	GCT	CCC	ACC	ATC	CGT	GCC	CTC	CAG	GAC	CCC	ACT	GAG	GTG	AAC	2256
	His	Tyr	Ala	Pro	Thr	Ile	Arg	Ala	Leu	Gln	Asp	Pro	Thr	Glu	Val	Asn	
		715				720					725					730	
65	GTC	GGG	GGT	TCT	GTG	GAC	ATA	GTC	TGC	ACT	GTC	GAT	GCC	AAT	CCC	ATC	2304
	Val	Gly	Gly	Ser	Val	Asp	Ile	Val	Cys	Thr	Val	Asp	Ala	Asn	Pro	Ile	
					735					740						745	

	CCC CAG GCC ACC ACC TTC ACG CTG ACT GGT CTA CAG CCT TCT ACA AGA	3024
	Pro Gln Ala Thr Thr Phe Thr Leu Thr Gly Leu Gln Pro Ser Thr Arg	
	975 980 985	
5	TAC AGG GTC TGG CTG CTG GCC AGT AAT GCC TTG GGG GAC AGT GGA CTG	3072
	Tyr Arg Val Trp Leu Leu Ala Ser Asn Ala Leu Gly Asp Ser Gly Leu	
	990 995 1000	
10	GCT GAC AAA GGG ACC CAG CTT CCC ATC ACT ACC CCA GGT CTC CAC CAG	3120
	Ala Asp Lys Gly Thr Gln Leu Pro Ile Thr Thr Pro Gly Leu His Gln	
	1005 1010 1015	
15	CCT TCT GGA GAA CCT GAA GAC CAG CTG CCC ACA GAG CCA CCT TCA GGA	3168
	Pro Ser Gly Glu Pro Glu Asp Gln Leu Pro Thr Gly Pro Pro Ser Gly	
	1020 1025 1030	
20	CCC TCG GGG CTG CCC CTG CTG CCT GTG CTG TTC GCT CTT GGG GGG CTT	3216
	Pro Ser Gly Leu Pro Leu Leu Pro Val Leu Phe Ala Leu Gly Gly Leu	
	1035 1040 1045 1050	
25	CTG CTC CTC TCC AAT GCC TCC TGT GTC GGG GGG GTC CTC TGG CAG CGG	3264
	Leu Leu Leu Ser Asn Ala Ser Cys Val Gly Gly Val Leu Trp Gln Arg	
	1055 1060 1065	
30	AGA CTC AGG CGT CTT GCT GAG GGC ATC TCA GAG AAG ACA GAG GCA GGG	3312
	Arg Leu Arg Arg Leu Ala Glu Gly Ile Ser Glu Lys Thr Glu Ala Gly	
	1070 1075 1080	
35	TCG GAA GAG GAC CGA GTC AGG AAC GAA TAT GAG GAG AGC CAG TGG ACA	3360
	Ser Glu Glu Asp Arg Val Arg Asn Glu Tyr Glu Glu Ser Gln Trp Thr	
	1085 1090 1095	
40	GGA GAG CGG GAC ACT CAG AGC TCC ACG GTC AGC ACA ACA GAG GCA GAG	3408
	Gly Glu Arg Asp Thr Gln Ser Ser Thr Val Ser Thr Thr Glu Ala Glu	
	1100 1105 1110	
45	CCG TAT TAC CGC TCC CTG AGG GAC TTC AGC CCC CAG CTG CCC CCG ACG	3456
	Pro Tyr Tyr Arg Ser Leu Arg Asp Phe Ser Pro Gln Leu Pro Pro Thr	
	1115 1120 1125 1130	
50	CAG GAG GAG GTG TCT TAT TCC CGA GGT TTC ACA GGT GAA GAT GAG GAT	3504
	Gln Glu Glu Val Ser Tyr Ser Arg Gly Phe Thr Gly Glu Asp Glu Asp	
	1135 1140 1145	
55	ATG GCC TTC CCT GGG CAC TTG TAT GAT GAG GTA GAA AGA ACG TAC CCC	3552
	Met Ala Phe Pro Gly His Leu Tyr Asp Glu Val Glu Arg Thr Tyr Pro	
	1150 1155 1160	
60	CCG TCT GGA GCC TGG GGA CCC CTC TAC GAT GAA GTG CAG ATG GGA CCC	3600
	Pro Ser Gly Ala Trp Gly Pro Leu Tyr Asp Glu Val Gln Met Gly Pro	
	1165 1170 1175	
65	TGG GAC CTC CAC TGG CCT GAA GAC ACA TAT CAG GAT CCA AGA GGA ATC	3648
	Trp Asp Leu His Trp Pro Glu Asp Thr Tyr Gln Asp Pro Arg Gly Ile	
	1180 1185 1190	

TAT GAC CAG GTG GCC GGA GAC TTG GAC ACT CTG GAA CCC GAT TCT CTG 3696
 Tyr Asp Gln Val Ala Gly Asp Leu Asp Thr Leu Glu Pro Asp Ser Leu
 1195 1200 1205 1210

5 CCC TTC GAG CTG AGG GGA CAT CTG GTG TAAGAGCCCT CTCAACCCCA 3743
 Pro Phe Glu Leu Arg Gly His Leu Val
 1215

10 TTGTCCTGCA CCTGCAGGAA TTTACACTCC ACTGGTCTCT CTCATTACAG CCTGGGCCGA 3803
 GCTGGTTAGG TGAGCTCCAT AAAACCCAAA GGGACTTGGT GTCAGGAGAG GACATGGAGG 3863
 GGGCTGAGTG ACAGAGATGG TTCAGCTGGT ACCAGAGTAG AAACAAGGTG CATCCTGGGG 3923

15 TTGGCTTTAG AAATAAACT TCTCCAAAAG GACAGGGCAG ATTGTAAACG TCGTCTCAAA 3983
 AATGAAATGC TGCCGGGTGC GGTGACTCAC GCCTATAATC CCAGCACTTT GGGAGGCTGA 4043
 GGCGGGTGGA TCACCTGAGG TCAGGAGTTC GAGACCAGCC TGGCCAACAT GGTAAAACTC 4103

20 CATTCTACT AAAAATATAA AAAATTAGCC AGGAGTAGTG GCGCATGCCT GTAGTCCCAG 4163
 CTACTTGGA GGCTGATGCA TGAGAATTGC TTGAACCCAG GAGGCGGAGG TTGCAGTGAG 4223

25 CTGAGATCAC GCCACTGCAC TCCAGCCTGG GCGACAGAGC GAGATTCTGT CTCAAAAAAT 4283
 AA 4285

30 (2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1241 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

40 Met Ala Leu Gly Thr Thr Leu Arg Ala Ser Leu Leu Leu Gly Leu
 -22 -20 -15 -10

45 Leu Thr Glu Gly Leu Ala Gln Leu Ala Ile Pro Ala Ser Val Pro Arg
 -5 1 5 10

Gly Phe Trp Ala Leu Pro Glu Asn Leu Thr Val Val Glu Gly Ala Ser
 15 20 25

50 Val Glu Leu Arg Cys Gly Val Ser Thr Pro Gly Ser Ala Val Gln Trp
 30 35 40

Ala Lys Asp Gly Leu Leu Leu Gly Pro Asp Pro Arg Ile Pro Gly Phe
 45 50 55

55 Pro Arg Tyr Arg Leu Glu Gly Asp Pro Ala Arg Gly Glu Phe His Leu
 60 65 70

His Ile Glu Ala Cys Asp Leu Ser Asp Asp Ala Glu Tyr Glu Cys Gln
 75 80 85 90
 5 Val Gly Arg Ser Glu Met Gly Pro Glu Leu Val Ser Pro Arg Val Ile
 95 100 105
 Leu Ser Ile Leu Val Pro Pro Lys Leu Leu Leu Leu Thr Pro Glu Ala
 110 115 120
 10 Gly Thr Met Val Thr Trp Val Ala Gly Gln Glu Tyr Val Val Asn Cys
 125 130 135
 Val Ser Gly Asp Ala Lys Pro Ala Pro Asp Ile Thr Ile Leu Leu Ser
 140 145 150
 15 Gly Gln Thr Ile Ser Asp Ile Ser Ala Asn Val Asn Glu Gly Ser Gln
 155 160 165 170
 20 Gln Lys Leu Phe Thr Val Glu Ala Thr Ala Arg Val Thr Pro Arg Ser
 175 180 185
 Ser Asp Asn Arg Gln Leu Leu Val Cys Glu Ala Ser Ser Pro Ala Leu
 190 195 200
 25 Glu Ala Pro Ile Lys Ala Ser Phe Thr Val Asn Val Leu Phe Pro Pro
 205 210 215
 Gly Pro Pro Val Ile Glu Trp Pro Gly Leu Asp Glu Gly His Val Arg
 220 225 230
 30 Ala Gly Gln Ser Leu Glu Leu Pro Cys Val Ala Arg Gly Gly Asn Pro
 235 240 245 250
 35 Leu Ala Thr Leu Gln Trp Leu Lys Asn Gly Gln Pro Val Ser Thr Ala
 255 260 265
 Trp Gly Thr Glu His Thr Gln Ala Val Ala Arg Ser Val Leu Val Met
 270 275 280
 40 Thr Val Arg Pro Glu Asp His Gly Ala Gln Leu Ser Cys Glu Ala His
 285 290 295
 Asn Ser Val Ser Ala Gly Thr Gln Glu His Gly Ile Thr Leu Gln Val
 300 305 310
 Thr Phe Pro Pro Ser Ala Ile Ile Ile Leu Gly Ser Ala Ser Gln Thr
 315 320 325 330
 50 Glu Asn Lys Asn Val Thr Leu Ser Cys Val Ser Lys Ser Ser Arg Pro
 335 340 345
 Arg Val Leu Leu Arg Trp Trp Leu Gly Trp Arg Gln Leu Leu Pro Met
 350 355 360
 55 Glu Glu Thr Val Met Asp Gly Leu His Gly Gly His Ile Ser Met Ser
 365 370 375

	Asn	Leu	Thr	Phe	Leu	Ala	Arg	Arg	Glu	Asp	Asn	Gly	Leu	Thr	Leu	Thr	
	380						385					390					
5	Cys	Glu	Ala	Phe	Ser	Glu	Ala	Phe	Thr	Lys	Glu	Thr	Phe	Lys	Lys	Ser	
	395					400					405					410	
	Leu	Ile	Leu	Asn	Val	Lys	Tyr	Pro	Ala	Gln	Lys	Leu	Trp	Ile	Glu	Gly	
					415					420					425		
10	Pro	Pro	Glu	Gly	Gln	Lys	Leu	Arg	Ala	Gly	Thr	Arg	Val	Arg	Leu	Val	
				430					435					440			
	Cys	Leu	Ala	Ile	Gly	Gly	Asn	Pro	Glu	Pro	Ser	Leu	Met	Trp	Tyr	Lys	
15			445					450					455				
	Asp	Ser	Arg	Thr	Val	Thr	Glu	Ser	Arg	Leu	Pro	Gln	Glu	Ser	Arg	Arg	
	460						465					470					
20	Val	His	Leu	Gly	Ser	Val	Glu	Lys	Ser	Gly	Ser	Thr	Phe	Ser	Arg	Glu	
	475					480					485					490	
	Leu	Val	Leu	Val	Thr	Gly	Pro	Ser	Asp	Asn	Gln	Ala	Lys	Phe	Thr	Cys	
					495					500					505		
25	Lys	Ala	Gly	Gln	Leu	Ser	Ala	Ser	Thr	Gln	Leu	Ala	Val	Gln	Phe	Pro	
				510					515					520			
	Pro	Thr	Asn	Val	Thr	Ile	Leu	Ala	Asn	Ala	Ser	Ala	Leu	Arg	Pro	Gly	
30			525					530					535				
	Asp	Ala	Leu	Asn	Leu	Thr	Cys	Val	Ser	Val	Ser	Ser	Asn	Pro	Pro	Val	
	540						545					550					
35	Asn	Leu	Ser	Trp	Asp	Lys	Glu	Gly	Glu	Arg	Leu	Glu	Gly	Val	Ala	Ala	
	555					560					565					570	
	Pro	Pro	Arg	Arg	Ala	Pro	Phe	Lys	Gly	Ser	Ala	Ala	Ala	Arg	Ser	Val	
					575					580					585		
40	Leu	Leu	Gln	Val	Ser	Ser	Arg	Asp	His	Gly	Gln	Arg	Val	Thr	Cys	Arg	
				590					595					600			
	Ala	His	Ser	Ala	Glu	Leu	Arg	Glu	Thr	Val	Ser	Ser	Phe	Tyr	Arg	Leu	
45			605					610					615				
	Asn	Val	Leu	Tyr	Arg	Pro	Glu	Phe	Leu	Gly	Glu	Gln	Val	Leu	Val	Val	
							620		625			630					
50	Thr	Ala	Val	Glu	Gln	Gly	Glu	Ala	Leu	Leu	Pro	Val	Ser	Val	Ser	Ala	
	635					640					645					650	
	Asn	Pro	Ala	Pro	Glu	Ala	Phe	Asn	Trp	Thr	Phe	Arg	Gly	Tyr	Arg	Leu	
					655					660					665		
55	Ser	Pro	Ala	Gly	Gly	Pro	Arg	His	Arg	Ile	Leu	Ser	Ser	Gly	Ala	Leu	
				670					675					680			

His Leu Trp Asn Val Thr Arg Ala Asp Asp Gly Leu Tyr Gln Leu His
 685 690 695

5 Cys Gln Asn Ser Glu Gly Thr Ala Glu Ala Arg Leu Arg Leu Asp Val
 700 705 710

His Tyr Ala Pro Thr Ile Arg Ala Leu Gln Asp Pro Thr Glu Val Asn
 715 720 725 730

10 Val Gly Gly Ser Val Asp Ile Val Cys Thr Val Asp Ala Asn Pro Ile
 735 740 745

Leu Pro Gly Met Phe Asn Trp Glu Arg Leu Gly Glu Asp Glu Glu Asp
 750 755 760

Gln Ser Leu Asp Asp Met Glu Lys Ile Ser Arg Gly Pro Thr Gly Arg
 765 770 775

20 Leu Arg Ile His His Ala Lys Leu Ala Gln Ala Gly Ala Tyr Gln Cys
 780 785 790

Ile Val Asp Asn Gly Val Ala Pro Pro Ala Arg Arg Leu Leu Arg Leu
 795 800 805 810

25 Val Val Arg Phe Ala Pro Gln Val Glu His Pro Thr Pro Leu Thr Lys
 815 820 825

Val Ala Ala Ala Gly Asp Ser Thr Ser Ser Ala Thr Leu His Cys Arg
 830 835 840

Ala Arg Gly Val Pro Asn Ile Val Phe Thr Trp Thr Lys Asn Gly Val
 845 850 855

35 Pro Leu Asp Leu Gln Asp Pro Arg Tyr Thr Glu His Thr Tyr His Gln
 860 865 870

Gly Gly Val His Ser Ser Leu Leu Thr Ile Ala Asn Val Ser Ala Ala
 875 880 885 890

40 Gln Asp Tyr Ala Leu Phe Thr Cys Thr Ala Thr Asn Ala Leu Gly Ser
 895 900 905

Asp Gln Thr Asn Ile Gln Leu Val Ser Ile Ser Arg Pro Asp Pro Pro
 910 915 920

Ser Gly Leu Lys Val Val Ser Leu Thr Pro His Ser Val Gly Leu Glu
 925 930 935

50 Trp Lys Pro Gly Phe Asp Gly Gly Leu Pro Gln Arg Phe Cys Ile Arg
 940 945 950

Tyr Glu Ala Leu Gly Thr Pro Gly Phe His Tyr Val Asp Val Val Pro
 955 960 965 970

55 Pro Gln Ala Thr Thr Phe Thr Leu Thr Gly Leu Gln Pro Ser Thr Arg
 975 980 985

Tyr Arg Val Trp Leu Leu Ala Ser Asn Ala Leu Gly Asp Ser Gly Leu
 990 995 1000
 5 Ala Asp Lys Gly Thr Gln Leu Pro Ile Thr Thr Pro Gly Leu His Gln
 1005 1010 1015
 Pro Ser Gly Glu Pro Glu Asp Gln Leu Pro Thr Glu Pro Pro Ser Gly
 1020 1025 1030
 10 Pro Ser Gly Leu Pro Leu Leu Pro Val Leu Phe Ala Leu Gly Gly Leu
 1035 1040 1045 1050
 Leu Leu Leu Ser Asn Ala Ser Cys Val Gly Gly Val Leu Trp Gln Arg
 15 1055 1060 1065
 Arg Leu Arg Arg Leu Ala Glu Gly Ile Ser Glu Lys Thr Glu Ala Gly
 1070 1075 1080
 20 Ser Glu Glu Asp Arg Val Arg Asn Glu Tyr Glu Glu Ser Gln Trp Thr
 1085 1090 1095
 Gly Glu Arg Asp Thr Gln Ser Ser Thr Val Ser Thr Thr Glu Ala Glu
 1100 1105 1110
 25 Pro Tyr Tyr Arg Ser Leu Arg Asp Phe Ser Pro Gln Leu Pro Pro Thr
 1115 1120 1125 1130
 Gln Glu Glu Val Ser Tyr Ser Arg Gly Phe Thr Gly Glu Asp Glu Asp
 30 1135 1140 1145
 Met Ala Phe Pro Gly His Leu Tyr Asp Glu Val Glu Arg Thr Tyr Pro
 1150 1155 1160
 35 Pro Ser Gly Ala Trp Gly Pro Leu Tyr Asp Glu Val Gln Met Gly Pro
 1165 1170 1175
 Trp Asp Leu His Trp Pro Glu Asp Thr Tyr Gln Asp Pro Arg Gly Ile
 1180 1185 1190
 40 Tyr Asp Gln Val Ala Gly Asp Leu Asp Thr Leu Glu Pro Asp Ser Leu
 1195 1200 1205 1210
 Pro Phe Glu Leu Arg Gly His Leu Val
 45 1215

(2) INFORMATION FOR SEQ ID NO:3:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 55 (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "primer exon 2 5'UTR"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

5 GAGAAAGCCA GACAGACGCA G

21

(2) INFORMATION FOR SEQ ID NO:4:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer intron 2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

20 AGCTTCCGCT GGTGGCT

17

(2) INFORMATION FOR SEQ ID NO:5:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer intron 23"

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTCGGGGAGA CCCACCC

17

(2) INFORMATION FOR SEQ ID NO:6:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer intron 26"

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

55 CCTGATGCTA ACGGCAGGGC

20